BEST AVAILABLE COPY RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/040,949

Source 0196

Date Processed by STIC: 9/18/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or.
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS; PLEASE CONTACT MARK SPENCER; 703±3084212

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX; 703-308-4216.

PATENTIN'2:1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax),

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER WERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- 3. Hand Carry directly to:
 - U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
 - U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
- 4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



OIPE

RAW SEQUENCE LISTING

DATE: 09/18/2002 TIME: 14:46:57

PATENT APPLICATION: US/10/040,949

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09182002\J040949.raw

```
3 <110> APPLICANT: Introgene BV
             Havenga, Menzo
             Vogels, Ronald
     5
     7 <120> TITLE OF INVENTION: Infection with chimaeric adenoviruses of cells negative
            for the adenovirus serotype 5 Coxsacki adenovirus
             receptor (CAR)
    11 <130> FILE REFERENCE: 2183-52226US
    13 <140> CURRENT APPLICATION NUMBER: 10/040,949
                                                                   Does Not Combly
C--> 14 <141> CURRENT FILING DATE: 2002-09-09
                                                               Corrected Diskette Needed
    16 <150> PRIOR APPLICATION NUMBER: WOO1/04334
    17 <151> PRIOR FILING DATE: 2000-07-07
    19 <150> PRIOR APPLICATION NUMBER: EP 99202234.3
    20 <151> PRIOR FILING DATE: 1999-07-08
                                                                    enow
throughout
    22 <150> PRIOR APPLICATION NUMBER: US 60/142,557
    23 <151> PRIOR FILING DATE: 2000-07-07
     25 <160> NUMBER OF SEQ ID NOS: 58
     27 <170> SOFTWARE: PatentIn version 3.1
```

ERRORED SEQUENCES

```
94 <210> SEO ID NO: 5
     95 <211> LENGTH: 64
     96 <212> TYPE: DNA
     97 <213> ORGANISM: Artificial Sequence
     99 <220> FEATURE:
     100 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
     102 <220> FEATURE:
     103 <221> NAME/KEY: misc_feature
     104 <222> LOCATION: (1)..(64)
     105 <223> OTHER INFORMATION: primer LRT-2
     107 <400> SEQUENCE: 5
E--> 108 gcggatcctt cgaaccatgg taagcttggt accgctagcg ttaaccgggc 7
     109/gactcagtca
     111 atcg
     614 <210> SEQ ID NO: 30
     615 <211> LENGTH: 377
     616 <212> TYPE: PRT
     617 <213> ORGANISM: adenoviridae
     619 <220> FEATURE:
     620 <221> NAME/KEY: VARIANT
     621 <222> LOCATION: (1)..(377)
```

622 <223> OTHER INFORMATION: Serotype 8 fiber protein

more group one
bases up one
line. More
cumulative
base total
up one line.

Cumulative base
total must be at
ught margin 9/18/02
ob each line.

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\09182002\J040949.raw

624 <400> SEQUENCE: 30 626 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met E--> 627 1 630 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr 25 634 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val 40 638 Ser Ser Asn Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys 55 642 Leu Ala Asp Pro Ile Thr Ile Asn Asn Gln Asn Val Ser Leu Lys Val 70 75 646 Gly Gly Leu Thr Leu Gln Glu Glu Thr Gly Lys Leu Thr Val Asn 85 90 650 Thr Glu Pro Pro Leu His Leu Thr Asn Asn Lys Leu Gly Ile Ala Leu 651 100 105 110 654 Asp Ala Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala Gly 120 125 658 His Gly Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly Leu 135 130 662 Val Asn Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Asp Leu 155 145 666 Ser Asn Asn Gly Gly Asn Ile Cys Val Arg Val Gly Glu Gly Gly Gly 170 670 Leu Ser Phe Asn Asp Asn Gly Asp Leu Val Ala Phe Asn Lys Lys Glu 180 185 674 Asp Lys Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Arg 195 200 678 Ile Asp Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys E--> 679 210 215 682 Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Arg E--> 683 225 230 235 686 Tyr Lys Ile Ile Asn Asn Thr Asn Pro Ala Leu Lys Gly Phe Thr 245 250 690 Ile Lys Leu Phe Asp Lys Asn Gly Val Leu Met Glu Ser Ser Asn 260 265 E--> 691 694 Leu Gly Lys Ser Tyr Trp Asn Phe Arg Asn Gln Asn Ser Ile Met Ser 280 698 Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr 290 295 702 Pro Lys Pro Thr Thr Gly Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr E--> 703 305 310 315 706 Gly Asn Ile Tyr Leu Gly Gly Lys Pro His Gln Pro Val Thr Ile Lys E--> 707325 330 710 Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asp E--> 711 340 345 714 Phe Ser Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr Ser E--> 715 355 718 Phe Thr Phe Ser Tyr Ile Ala Gln Glu

370

375

E--> 719

RAW SEQUENCE LISTING

DATE: 09/18/2002

PATENT APPLICATION: US/10/040,949 TIME: 14:46:57

Input Set : A:\Sequence Listing.txt Output Set: N:\CRF4\09182002\J040949.raw

721 <210> SEQ ID NO: 31 722 <211> LENGTH: 377 723 <212> TYPE: PRT

724 <213> ORGANISM: adenoviridae

727 <220> FEATURE:

728 <221> NAME/KEY: VARIANT 729 <222> LOCATION: (1)..(377)

730 <223> OTHER INFORMATION: Serotype 9 fiber protein

734 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met 735

E--> 735

738 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr 20 25

742 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val 40

746 Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys 55

750 Leu Ala Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val

70

754 Gly Gly Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val Asn 85

758 Ala Asp Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala Leu 100 105

762 Asp Ala Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala Gly 115 120

766 His Gly Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly Leu 135

770 Ile Asn Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Ser 150 155

774 Thr Asp Asn Gly Gly Ser Val Cys Val Arg Val Gly Glu Gly Gly Gly

165 170 778 Leu Ser Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys Glu

180 185 782 Asp Lys Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys

195 200 205 786 Ile Asp Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys

215 220

790 Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys 230 235

794 Tyr Lys Ile Ile Asn Asn Asn Thr Gln Pro Ala Leu Lys Gly Phe Thr 245 250

798 Ile Lys Leu Leu Phe Asp Glu Asn Gly Val Leu Met Glu Ser Ser Asn 799 260 265

802 Leu Gly Lys Ser Tyr Trp Asn Phe Arg Asn Glu Asn Ser Ile Met Ser

280

806 Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr 295 300

810 Pro Lys Pro Thr Ala Gly Ser Lys Lys Tyr Ala Arg Asp lle Val Tyr 811 305 310 315

DATE: 09/18/2002

TIME: 14:46:57

```
PATENT APPLICATION: US/10/040,949
                     Input Set : A:\Sequence Listing.txt
                    Output Set: N:\CRF4\09182002\J040949.raw
    814 Gly Asn Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Val Thr Ile Lys
                                             330
    818 Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asp
                                         345
                    340
    819
    822 Phe Ser Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr Ser
                                                         365
                355
                                     360
    826 Phe Thr Phe Ser Tyr Ile Ala Gln Glu
            370
                                 375
    829 <210> SEQ ID NO: 32
    830 <211> LENGTH: 391
     831 <212> TYPE: PRT
     832 <213> ORGANISM: adenoviridae
     834 <220> FEATURE:
     835 <221> NAME/KEY: VARIANT
     836 <222> LOCATION: (1)..(391)
     837 <223> OTHER INFORMATION: Serotype 13 fiber protein
     839 <220> FEATURE:
     840 <221> NAME/KEY: MISC_FEATURE
    841 <222> LOCATION: (1)..(5)
     842 <223> OTHER INFORMATION: 'Xaa' at positions 1-5 indicates an unidentified amino
              acid due to unidentified nucleotide(s)
     845 <220> FEATURE:
     846 <221> NAME/KEY: MISC_FEATURE
     847 <222> LOCATION: (23)
     848 <223> OTHER INFORMATION: 'Xaa' at position 23 indicates an unidentified amino acid
               due to unidentified nucleotide(s)
     849
     851 <220> FEATURE:
     852 <221> NAME/KEY: MISC_FEATURE
     853 <222> LOCATION: (41)
    854 <223> OTHER INFORMATION: 'Xaa' at position 41 indicates an unidentified amino acid
              due to unidentified nucleotide(s)
     857 <220> FEATURE:
     858 <221> NAME/KEY: MISC_FEATURE
     859 <222> LOCATION: (43)
     860 <223> OTHER INFORMATION: 'Xaa' at position 43 indicates an unidentified amino acid
               due to unidentified nucleotide(s)
     861
     863 <220> FEATURE:
     864 <221> NAME/KEY: MISC_FEATURE
     865 <222> LOCATION: (49)
     866 <223> OTHER INFORMATION: 'Xaa' at position 49 indicates an unidentified amino acid
               due to unidentified nucleotide(s)
     867
     869 <220> FEATURE:
     870 <221> NAME/KEY: MISC_FEATURE
     871 <222> LOCATION: (385)
     872 <223> OTHER INFORMATION: 'Xaa' at position 385 indicates an unidentified amino acid
               due to unidentified nucleotide(s)
     875 <400> SEQUENCE: 32
W--> 877 Xaa Xaa Xaa Xaa Xaa Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
E--> 878
                                                                          5
```

RAW SEQUENCE LISTING

same eno

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\09182002\J040949.raw

W--> 881 Lys Arg Ala Arg Ser Ser Xaa Asp Thr Phe Asn Pro Val Tyr Pro Tyr 885 Gly Tyr Ala Arg Asn Gln Asn Ile Xaa Phe Xaa Thr Pro Pro Phe Val --> 889 Xaa Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys 893 Leu Ala Asp Pro Ile Thr Ile Ala Asn Gly Asp Val Ser Leu Lys Val 897 Gly Gly Gly Leu Thr Leu Gln Glu Gly Ser Leu Thr Val Asp Pro Lys 901 Ala Pro Leu Gln Leu Ala Asn Asp Lys Lys Leu Glu Leu Val Tyr Asp 905 Asp Pro Phe Glu Val Ser Thr Asn Lys Leu Ser Leu Lys Val Gly His 909 Gly Leu Lys Val Leu Asp Asp Lys Ser Ala Gly Gly Leu Lys Asp Leu 913 Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Ile Glu Asn 917 Leu Gln Asn Asp Asp Gly Ser Ser Arg Gly Val Gly Ile Asn Val Arg 921 Leu Gly Thr Asp Gly Gly Leu Ser Phe Asp Arg Lys Gly Glu Leu Val 925 Ala Trp Asn Arg Lys Asp Asp Arg Thr Leu Trp Thr Thr Pro Asp 195 . 929 Pro Ser Pro Asn Cys Lys Ala Glu Thr Glu Lys Asp Ser Lys Leu Thr 933 Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Ile 937 Ile Val Leu Lys Gly Lys Tyr Glu Phe Val Lys Lys Glu Thr Glu Pro 941 Lys Ser Phe Asp Val Lys Leu Leu Phe Asp Ser Lys Gly Val Leu Leu 945 Pro Thr Ser Asn Leu Ser Lys Glu Tyr Trp Asn Tyr Arg Ser Tyr Asp 949 Asn Asn Ile Gly Thr Pro Tyr Glu Asn Ala Val Pro Phe Met Pro Asn 953 Leu Lys Ala Tyr Pro Lys Pro Thr Lys Thr Ala Ser Asp Lys Ala Glu 957 Asn Lys Ile Ser Ser Ala Lys Asn Lys Ile Val Ser Asn Phe Tyr Phe 961 Gly Gly Gln Ala Tyr Gln Pro Gly Thr Ile Ile Ile Lys Phe Asn Glu 965 Glu Ile Asp Glu Thr Cys Ala Tyr Ser Ile Thr Phe Asn Phe Gly Trp 969 Gly Lys Val Tyr Asp Asn Pro Phe Pro Phe Asp Thr Thr Ser Phe Thr 973 Xaa Ser Tyr Ile Ala Gln Glu 976 <210> SEQ ID NO: 33

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\09182002\J040949.raw

```
977 <211> LENGTH: 290
    978 <212> TYPE: PRT
    979 <213> ORGANISM: adenoviridae
    981 <220> FEATURE:
    982 <221> NAME/KEY: VARIANT
    983 <222> LOCATION: (1)..(290)
    984 <223> OTHER INFORMATION: Serotype 14 fiber protein
    986 <400> SEQUENCE: 33
    988 His Pro Phe Ile Asn Pro Gly Phe Ile Ser Pro Asn Gly Phe Thr Gln
E--> 989
                                                                                           10
                                                      1
     992 Ser Pro Asp Gly Val Leu Thr Leu Lys Cys Leu Thr Pro Leu Thr
                     20
     996 Thr Gly Gly Ser Leu Gln Leu Lys Val Gly Gly Gly Leu Thr Val Asp
                35
                                     40
     997
     1000 Asp Thr Asp Gly Thr Leu Gln Glu Asn Ile Gly Ala Thr Thr Pro Leu
                                  55
     1004 Val Lys Thr Gly His Ser Ile Gly Leu Ser Leu Gly Ala Gly Leu Gly
                                                  75
                             70
     1008 Thr Asp Glu Asn Lys Leu Cys Thr Lys Leu Gly Glu Gly Leu Thr Phe
                                              90
                          85
     1012 Asn Ser Asn Asn Ile Cys Ile Asp Asp Asn Ile Asn Thr Leu Trp Thr
                     100
                                         105
     1016 Gly Val Asn Pro Thr Glu Ala Asn Cys Gln Met Met Asp Ser Ser Glu
                                      120
     1017 115
     1020 Ser Asn Asp Cys Lys Leu Ile Leu Thr Leu Val Lys Thr Gly Ala Leu
                                                      140
                                 135
     1024 Val Thr Ala Phe Val Tyr Val Ile Gly Val Ser Asn Asn Phe Asn Met
                              150
     1028 Leu Thr Thr Tyr Arg Asn Ile Asn Phe Thr Ala Glu Leu Phe Phe Asp
                                              170
                          165
     1029
     1032 Ser Ala Gly Asn Leu Leu Thr Ser Leu Ser Ser Leu Lys Thr Pro Leu
                                          185
                     180
     1036 Asn His Lys Ser Gly Gln Thr Trp Leu Leu Val Pro Leu Leu Met Leu
                                      200
                195
     1040 Lys Val Ser Cys Pro Ala Gln Leu Leu Ile Leu Ser Ile Ile Ile Leu
                                  215
           210
     1045 Glu Lys Asn Lys Thr Thr Phe Thr Glu Leu Val Thr Thr Gln Leu Val
                              230
                                                  235
     1049 Ile Thr Leu Leu Phe Pro Leu Thr Ile Ser Val Met Leu Asn Gln Arg
                          245
                                              250
     1053 Ala Ile Arg Ala Asp Thr Ser Tyr Cys Ile Arg Ile Thr Trp Ser Trp
                                                              270
                                          265
                      260
     1057 Asn Thr Gly Asp Ala Pro Glu Gly Gln Thr Ser Ala Thr Thr Leu Val
                                      280
     1058
                  275
     1061 Thr Ser
     1062
              290
     1064 <210> SEQ ID NO: 34
     1065 <211> LENGTH: 345
```

1066 <212> TYPE: PRT

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\09182002\J040949.raw

```
1067 <213> ORGANISM: adenoviridae
    1069 <220> FEATURE:
    1070 <221> NAME/KEY: VARIANT
    1071 <222> LOCATION: (1)..(345)
    1072 <223> OTHER INFORMATION: Serotype 20 fiber protein
    1074 <400> SEQUENCE: 34
    1076 Ile Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser Asp Gly
E--> 1077
    1080 Leu Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala Asp Pro
                                        25
    1084 Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val Gly Gly Ile
                                    40
    1088 Thr Val Glu Gln Asp Ser Gly Gln Leu Ile Ala Asn Pro Lys Ala Pro
                                55
    1092 Leu Gln Val Ala Asn Asp Lys Leu Glu Leu Ser Tyr Ala Tyr Pro Phe
                            70
    1096 Glu Thr Ser Ala Asn Lys Leu Ser Leu Lys Val Gly Gln Gly Leu Lys
                                            90
                        85
    1100 Val Leu Asp Glu Lys Asp Ser Gly Gly Leu Gln Asn Leu Leu Gly Lys
           100
                                       105
    1104 Leu Val Val Leu Thr Gly Lys Gly Ile Gly Val Glu Glu Leu Lys Asn
                                                        125
                                    120
    1105 115
    1108 Pro Asp Asn Thr Asn Arg Gly Val Gly Ile Asn Val Arg Leu Gly Lys
                                135
             130
    1112 Asp Gly Gly Leu Ser Phe Asn Lys Asn Gly Glu Leu Val Ala Trp Asn
                            150
                                                155
    1116 Lys His Asn Asp Thr Gly Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro
                                            170
                        165
    1120 Asn Cys Lys Ile Glu Glu Val Lys Asp Ser Lys Leu Thr Leu Val Leu
                                       185
    1124 Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Met Ala Phe Gln Val Val
    1125 195
                                    200
    1128 Lys Gly Thr Tyr Glu Asn Ile Ser Lys Asn Thr Ala Lys Asn Ser Phe
                                215
                                                    220
    1129 210
    1132 Ser Ile Lys Leu Leu Phe Asp Asp Asn Gly Lys Leu Leu Glu Gly Ser
                            230 · 235
    1136 Ser Leu Asp Lys Asp Tyr Trp Asn Phe Arg Ser Asp Asp Ser Ile Ile
                         245
                                            250
    1140 Pro Asn Gln Tyr Asp Asn Ala Val Pro Phe Met Pro Asn Leu Lys Ala
                                                            270
                                        265
                     260
    1144 Tyr Pro Lys Pro Ser Thr Val Leu Pro Ser Thr Asp Lys Asn Ser Asn
                                    280
                275
    1148 Gly Lys Asn Thr Ile Val Ser Asn Leu Tyr Leu Glu Gly Lys Ala Tyr
                                 295
    1152 Gln Pro Val Ala Val Thr Ile Thr Phe Asn Lys Glu Ile Gly Cys Thr
                                               315
    1153 305
                             310
    1156 Tyr Ser Ile Thr Phe Asp Phe Gly Trp Ala Lys Thr Tyr Asp Val Pro
                         325
                                            330
    1157
```

1160 Ile Pro Phe Asp Ser Ser Ser Phe Thr

```
345
    1161
    1163 <210> SEQ ID NO: 35
    1164 <211> LENGTH: 346
    1165 <212> TYPE: PRT
    1166 <213> ORGANISM: adenoviridae
    1168 <220> FEATURE:
     1169 <221> NAME/KEY: VARIANT
    1170 <222> LOCATION: (1)..(346)
    1171 <223> OTHER INFORMATION: Serotype 23 fiber protein
    1173 <400> SEQUENCE: 35
    1175 Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser Asp Gly Phe
E--> 1176
                                                                                           10
                                                      1
    1179 Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala Asp Pro Ile
    1183 Ala Ile Thr Asn Gly Asp Val Ser Leu Lys Val Gly Gly Leu Thr
                                     40
    1187 Val Glu Gln Asp Ser Gly Asn Leu Lys Val Asn Thr Lys Ala Pro Leu
                                 55
    1191 Gln Val Ala Ala Asp Lys Gln Leu Glu Ile Ala Leu Ala Asp Pro Phe
                             70
    1195 Glu Val Ser Lys Gly Arg Leu Gly Ile Lys Ala Gly His Gly Leu Lys
                         85
                                             90
    1199 Val Ile Asp Asn Ser Ile Ser Gly Leu Glu Gly Leu Val Gly Thr Leu
                     100
    1203 Val Val Leu Thr Gly His Gly Ile Gly Thr Glu Asn Leu Leu Asn Asn
                                     120
    1207 Asp Gly Ser Ser Arg Gly Val Gly Ile Asn Val Arg Leu Gly Lys Asp
    1208 130
                                 135
    1211 Gly Gly Leu Ser Phe Asp Lys Lys Gly Asp Leu Val Ala Trp Asn Lys
                             150
                                                 155
    1215 Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn
                                             170
                         165
    1219 Cys Lys Val Ile Glu Ala Lys Asp Ser Lys Leu Thr Leu Val Leu Thr
                                         185
                     180
    1223 Lys Cys Gly Ser Gln Ile Leu Ala Asn Met Ser Leu Leu Ile Leu Lys
                195
                                     200
                                                         205
    1227 Gly Thr Tyr Glu Tyr Ile Ser Asn Ala Ile Ala Asn Lys Ser Phe Thr
                                 215
    1231 Ile Lys Leu Leu Phe Asn Asp Lys Gly Val Leu Met Asp Gly Ser Ser
                             230
                                                 235
    1235 Leu Asp Lys Asp Tyr Trp Asn Tyr Lys Ser Asp Asp Ser Val Met Ser
    1236
                                             250
                         245
    1239 Lys Ala Tyr Glu Asn Ala Val Pro Phe Met Pro Asn Leu Lys Ala Tyr
                     260
                                         265
    1243 Pro Asn Pro Thr Thr Ser Thr Thr Asn Pro Ser Thr Asp Lys Ser
           275
                                     280
    1247 Asn Gly Lys Asn Ala Ile Val Ser Asn Val Tyr Leu Glu Gly Arg Ala
             290
                                 295
    1251 Tyr Gln Pro Val Ala Ile Thr Ile Thr Phe Asn Lys Glu Thr Gly Cys
```

```
315
                             310
    1252 305
    1255 Thr Tyr Ser Met Thr Phe Asp Phe Gly Trp Ser Lys Val Tyr Asn Asp
                                      330
                     325
    1259 Pro Ile Pro Phe Asp Thr Ser Ser Leu Thr
    1260
                     340
    1262 <210> SEQ ID NO: 36
    1263 <211> LENGTH: 390
    1264 <212> TYPE: PRT
    1265 <213> ORGANISM: adenoviridae
    1267 <220> FEATURE:
    1268 <221> NAME/KEY: VARIANT
    1269 <222> LOCATION: (1)..(390)
    1270 <223> OTHER INFORMATION: Serotype 24 fiber protein
    1273 <400> SEQUENCE: 36
    1275 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
E--> 1276
                                                                                 10
                                             1
    1279 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
                                         25
                     20
    1283 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val
                                                          45
                 35
                                     40
    1287 Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
     1288
     1291 Leu Ala Asp Pro Ile Ala Ile Thr Asn Gly Asp Val Ser Leu Lys Val
                                                  75
                             70
     1292 65
     1295 Gly Gly Leu Thr Val Glu Lys Asp Ser Gly Asn Leu Lys Val Asn
                          85
    1299 Pro Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Gln Leu Glu Ile Ala
                                                              110
                                         105
                     100
     1303 Leu Ala Tyr Pro Phe Glu Val Ser Asn Gly Lys Leu Gly Ile Lys Ala
                                     120
     1304 115
     1307 Gly His Gly Leu Lys Val Ile Asp Lys Ile Ala Gly Leu Glu Gly Leu
                                                      140
            130
                                 135
     1311 Ala Gly Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Asn
                                                  155
                             150
     1315 Leu Glu Asn Ser Asp Gly Ser Ser Arg Gly Val Gly Ile Asn Val Arg
                                              170
                          165
     1319 Leu Ala Lys Asp Gly Gly Leu Ser Phe Asp Lys Lys Gly Asp Leu Val
                                          185
                     180
     1323 Ala Trp Asn Lys His Asp Asp Arg Arg Thr Leu Trp Thr Thr Pro Asp
                                      200
                 195
     1327 Pro Ser Pro Asn Cys Thr Ile Asp Gln Glu Arg Asp Ser Lys Leu Thr
                                  215
                                                      220
     1331 Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu
                              230
                                                  235
     1335 Leu Val Val Lys Gly Lys Phe Ser Asn Ile Asn Asn Asn Thr Asn Pro
     1336
                          245
                                              250
     1339 Thr Asp Lys Lys Ile Thr Val Lys Leu Leu Phe Asn Glu Lys Gly Val
                                          265
     1343 Leu Met Asp Ser Ser Thr Leu Lys Lys Glu Tyr Trp Asn Tyr Arg Asn
```

```
280
                 275
    1344
    1347 Asp Asn Ser Thr Val Ser Gln Ala Tyr Asp Asn Ala Val Pro Phe Met
                                 295
                                                      300
    1351 Pro Asn Ile Lys Ala Tyr Pro Lys Pro Thr Thr Asp Thr Ser Ala Lys
                                                  315
                              310
    1355 Pro Glu Asp Lys Lys Ser Ala Ala Lys Arg Tyr Ile Val Ser Asn Val
                                             330
                         325
    1359 Tyr Ile Gly Gly Leu Pro Asp Lys Thr Val Val Ile Thr Ile Lys Phe
                      340
                                         345
    1363 Asn Ala Glu Thr Glu Cys Ala Tyr Ser Ile Thr Phe Glu Phe Thr Trp
                                      360
    1364
                 355
     1367 Ala Lys Thr Phe Glu Asp Val Gln Phe Asp Ser Ser Ser Phe Thr Phe
    1368
             370
                                  375
                                                      380
    1371 Ser Tyr Ile Ala Gln Glu
    1372 385
    1374 <210> SEQ ID NO: 37
    1375 <211> LENGTH: 375
    1376 <212> TYPE: PRT
     1377 <213> ORGANISM: adenoviridae
    1379 <220> FEATURE:
    1380 <221> NAME/KEY: VARIANT
    1381 <222> LOCATION: (1)..(375)
    1382 <223> OTHER INFORMATION: Serotype 25 fiber protein
    1384 <220> FEATURE:
    1385 <221> NAME/KEY: MISC_FEATURE
     1386 <222> LOCATION: (141)
    1387 <223> OTHER INFORMATION: 'Xaa' at position 41 indicates an unidentified amino acid
               due to unidentified nucleotide(s)
     1390 <400> SEQUENCE: 37
    1392 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Gln Met
E--> 1393
                                                               5
     1396 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
    1397
                      20
                                          25
    1400 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val
                                                          45
                                      40
    1404 Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
                                  55
     1408 Leu Ala Asp Pro Ile Thr Ile Ser Asn Gly Asp Val Ser Leu Lys Val
                              70
    1412 Gly Gly Gly Leu Thr Val Glu Gln Asp Ser Gly Asn Leu Ser Val Asn
                                              90
                          85
    1416 Pro Lys Ala Pro Leu Gln Val Gly Thr Asp Lys Leu Glu Leu Ala
                      100
                                          105
     1420 Leu Ala Pro Pro Phe Asn Val Lys Asp Asn Lys Leu Asp Leu Leu Val
     1421
                 115
                                      120
                                                          125
   ▶ 1424 Gly Asp Gly Leu Lys Val Ile Asp Lys Ser Ile Ser Xaa Leu Pro Gly
            130
                                  135
                                                      140 .
     1428 Leu Leu Asn Tyr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Asn Glu
     1429 145
                              150
                                                  155
```

```
1432 Glu Leu Lys Asn Asp Asp Gly Ser Asn Lys Gly Val Gly Leu Cys Val
                         165
                                             170
     1436 Arg Ile Gly Glu Gly Gly Leu Thr Phe Asp Asp Lys Gly Tyr Leu
                                         185
    1440 Val Ala Trp Asn Lys Lys His Asp Ile Arg Thr Leu Trp Thr Thr Leu
          195
                                     200
    1444 Asp Pro Ser Pro Asn Cys Arg Ile Asp Val Asp Lys Asp Ser Lys Leu
                                 215
    1445 210
    1448 Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser
                             230
                                                 235
    1452 Leu Leu Val Val Lys Gly Arg Phe Gln Asn Leu Asn Tyr Lys Thr Asn
                         245
                                             250
    1453
     1456 Pro Asn Leu Pro Lys Thr Phe Thr Ile Lys Leu Leu Phe Asp Glu Asn
                                                             270
                     260
                                         265
     1457
    1460 Gly Ile Leu Lys Asp Ser Ser Asn Leu Asp Lys Asn Tyr Trp Asn Tyr
                                     280
          275
    1464 Arg Asn Gly Asn Ser Ile Leu Ala Glu Gln Tyr Lys Asn Ala Val Gly
                                 295
    1468 Phe Met Pro Asn Leu Ala Ala Tyr Pro Lys Ser Thr Thr Thr Gln Ser
                             310
                                                 315
    1472 Lys Leu Tyr Ala Arg Asn Thr Ile Phe Gly Asn Ile Tyr Leu Asp Ser
                         325
                                             330
    1473
    1476 Gln Ala Tyr Asn Pro Val Val Ile Lys Ile Thr Phe Asn Gln Glu Ala
                     340
                                         345
    1480 Asp Ser Ala Tyr Ser Ile Thr Leu Asn Tyr Ser Trp Gly Lys Asp Tyr
                                     360
    1481
                 355
     1484 Glu Asn Ile Pro Phe Asp Ser
     1485
             370
     1487 <210> SEQ ID NO: 38
     1488 <211> LENGTH: 335
     1489 <212> TYPE: PRT
    1490 <213> ORGANISM: adenoviridae
    1492 <220> FEATURE:
    1493 <221> NAME/KEY: VARIANT
    1494 <222> LOCATION: (1)..(335)
    1495 <223> OTHER INFORMATION: Serotype 27 fiber protein
    1497 <400> SEQUENCE: 38
    1499 Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys Asn
                                                                           same
E--> 1500
                                                                                 10
    1503 Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr Ile
                     20
    1507 Thr Asn Gly Asp Val Ser Leu Lys Val Gly Gly Leu Val Val Glu
    1511 Lys Glu Ser Gly Lys Leu Ser Val Asp Pro Lys Thr Pro Leu Gln Val
             50
                                 55
    1515 Ala Ser Asp Asn Lys Leu Glu Leu Ser Tyr Asn Ala Pro Phe Lys Val
    1519 Glu Asn Asp Lys Leu Ser Leu Asp Val Gly His Gly Leu Lys Val Ile
    1520
                         85
                                             90
```

```
1523 Gly Asn Glu Val Ser Ser Leu Pro Gly Leu Ile Asn Lys Leu Val Val
                                         105
                     100
    1527 Leu Thr Gly Lys Gly Ile Gly Thr Glu Glu Leu Lys Glu Gln Asn Ser
    1528 115
                                    120
                                                         125
    1531 Asp Lys Ile Ile Gly Val Gly Ile Asn Val Arg Ala Arg Gly Gly Leu
                                135
    1532 130
    1535 Ser Phe Asp Asn Asp Gly Tyr Leu Val Ala Trp Asn Pro Lys Tyr Asp
                            150
                                                 155
    1536 145
    1539 Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys Met
                                                                 175
                                             170
                        165
    1543 Leu Thr Lys Lys Asp Ser Lys Leu Thr Leu Thr Leu Thr Lys Cys Gly
                     180
                                         185
    1547 Ser Gln Ile Leu Gly Asn Val Ser Leu Leu Ala Val Ser Gly Lys Tyr
                                     200
    1548
                 195
    1551 Leu Asn Met Thr Lys Asp Glu Thr Gly Val Lys Ile Ile Leu Leu Phe
             210
                                 215
    1555 Asp Arg Asn Gly Val Leu Met Gln Glu Ser Ser Leu Asp Lys Glu Tyr
    1556 225
                             230
    1559 Trp Asn Tyr Arg Asn Asp Asn Asn Val Ile Gly Thr Pro Tyr Glu Asn
                         245
                                             250
    1563 Ala Val Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys Pro Thr Ser
                     260
                                         265
    1567 Ala Asp Ala Lys Asn Tyr Ser Arg Ser Lys Ile Ile Ser Asn Val Tyr
                                     280
                275
    1571 Leu Lys Gly Leu Ile Tyr Gln Pro Val Ile Ile Ile Ala Ser Phe Asn
                                 295
                                                      300
             290
    1575 Gln Glu Thr Thr Asn Gly Cys Val Tyr Ser Ile Ser Phe Asp Phe Thr
    1576 305
                             310
                                                 315
    1579 Cys Ser Lys Asp Tyr Thr Gly Gln Gln Phe Asp Val Thr Ser Phe
                                             330
                         325
    1582 <210> SEQ ID NO: 39
    1583 <211> LENGTH: 374
    1584 <212> TYPE: PRT
    1585 <213> ORGANISM: adenoviridae
    1589 <220> FEATURE:
    1590 <221> NAME/KEY: VARIANT
    1591 <222> LOCATION: (1)..(374)
    1592 <223> OTHER INFORMATION: Serotype 28 fiber protein
    1594 <400> SEQUENCE: 39
    1596 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
E--> 1597
                                                                                 10
                                                               5
    1600 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
                     20
                                         25
    1604 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val
                 35
                                     40
    1608 Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
                                 55
    1612 Leu Ala Asp Pro Ile Thr Ile Ala Asn Gly Asp Val Ser Leu Lys Leu
    1613 65
                                                 75
                             70
```

```
1616 Gly Gly Gly Leu Thr Val Glu Lys Glu Ser Gly Asn Leu Thr Val Asn
                          85
    1620 Pro Lys Ala Pro Leu Gln Val Ala Ser Gly Gln Leu Glu Leu Ala Tyr
                                         105
                     100
    1621
    1624 Tyr Ser Pro Phe Asp Val Lys Asn Asn Met Leu Thr Leu Lys Ala Gly
                 115
                                     120
    1628 His Gly Leu Ala Val Val Thr Lys Asp Asn Thr Asp Leu Gln Pro Leu
                                  135
                                                      140
             130
    1632 Met Gly Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Gly Thr
                                                  155
                             150
    1636 Ser Ala His Gly Gly Thr Ile Asp Val Arg Ile Gly Lys Asn Gly Ser
                                              170
    1637
                          165
    1640 Leu Ala Phe Asp Lys Asn Gly Asp Leu Val Ala Trp Asp Lys Glu Asn
    1641
                     180
    1644 Asp Arg Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys
           195
                                      200
    1648 Met Ser Glu Val Lys Asp Ser Lys Leu Thr Leu Ile Leu Thr Lys Cys
             210
                                  215
    1652 Gly Ser Gln Ile Leu Gly Ser Val Ser Leu Leu Ala Val Lys Gly Glu
                              230
                                                  235
    1656 Tyr Gln Asn Met Thr Ala Ser Thr Asn Lys Asn Val Lys Ile Thr Leu
                                              250
                          245
    1660 Leu Phe Asp Ala Asn Gly Val Leu Leu Glu Gly Ser Ser Leu Asp Lys
                                          265
                     260
    1664 Glu Tyr Trp Asn Phe Arg Asn Asn Asp Ser Thr Val Ser Gly Lys Tyr
                  275
                                      280
    1668 Glu Asn Ala Val Pro Phe Met Pro Asn Ile Thr Ala Tyr Lys Pro Val
                                  295
    1672 Asn Ser Lys Ser Tyr Ala Arg Ser His Ile Phe Gly Asn Val Tyr Ile
                              310
                                                  315
    1676 Asp Ala Lys Pro Tyr Asn Pro Val Val Ile Lys Ile Ser Phe Asn Gln
                                              330
                          325
    1681 Glu Thr Gln Asn Asn Cys Val Tyr Ser Ile Ser Phe Asp Tyr Thr Cys
                                       345
                     340
    1685 Ser Lys Glu Tyr Thr Gly Met Gln Phe Asp Val Thr Ser Phe Thr Phe
                                      360
                 355
    1689 Ser Tyr Ile Ala Gln Glu
             370
    1690
    1692 <210> SEQ ID NO: 40
     1693 <211> LENGTH: 343
    1694 <212> TYPE: PRT
     1695 <213> ORGANISM: adenoviridae
     1697 <220> FEATURE:
     1698 <221> NAME/KEY: VARIANT
     1699 <222> LOCATION: (1)..(343)
    1700 <223> OTHER INFORMATION: Serotype 29 fiber protein
     1702 <400> SEQUENCE: 40
    1704 Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser Asp Gly Phe
E--> 1705
                                                                                            15
                                                                        10
```

	1708	Lys	Asn	Phe		Pro	Gly	Val	Leu		Leu	Lys	Leu	Ala		Pro	Ile
E>	1709	_			20	~ 1	_		~	25	*	77- 7	C1	C1	30	T 011	Mhr
	1712	Ala	Ile		Asn	GLY	Asp	vaı		ьeu	ьуs	vaı	GTĀ		GLY	ьец	1111
E>	1713		_	35		_		_	40	_	1	•	D	45	21-	Dwa	T 0.11
	1716	Val		Gln	Asp	Ser	GLY		Leu	ser	vaı	Asn		гаг	Ата	PIO	ьeu
E>			50			_	_	55	_				60		D	D== =	Dho
	1720		Val	Gly	Thr	Asp		Lys	Leu	Glu	ьeu		ьeu	Ala	Pro	Pro	
E>	1721	65				_	70	_		-1	_	75	G1	3	~1	T 0.11	80
	1724	Asp	Val	Arg	Asp		Lys	Leu	Ala	TTE		vaı	GIY	Asp	GIY		гуз
E>	1725	_		_	_	85		_	_	.	90	01	T	т	3	95	T 011
	1728	Val	Ile	Asp		Ser	He	Ser	Asp		Pro	GIY	ьeu	ьeu		тАт	ьеи
E>				_	100		_			105		01	a 1	T	110	7 ~ ~	7 ~ ~
	1732	Val	Val		Thr	GLY	ьys	GTA		GIY	ASN	GIU	GIU		цуѕ	ASII	ASP
E>	1733	_		115	_	_	a 1	**- 1	120	Ŧ	a	77. 1	7 ~~	125	C1++	C1.,	C111
	1736	Asp		Ser	Asn	ьуs	GIY		GTĀ	ьeu	Cys	val		TIE	GIY	GIU	GIY
E>		~ .	130	-	m1	DI	3	135	T	c1	Merro	T 011	140	ת 1 ת	mrn.	λcn	λan
	1740		GTĀ	Leu	Thr	Pne		Asp	гуѕ	GTÄ	тут		Val	нта	пр	ASII	160
E>	1741			_		•	150	-	m	mh	mh m	155	7 an	Dro	cor	Dro	
	1744	гаг	HIS	Asp	TTE		THE	ьeu	ттр	TIII	170	ьец	ASP	PIO	261	175	A511
E>	1745		Ť	T10	7.00	165	C1.1	T	N an	Car		T.011	Thr	T. 2 11	Val		Thr
		Cys	гуѕ	ire	180	116	GIU	тур	АБР	185	пуз	цец	1111	пси	190	шеч	1111
E>	1749	Tvva	CTTC	C117		Cln	Tla	T.e.u	7. l a		Val	Ser	T.eu	Tle		Val	Asn
п 🔪		пåг	Суѕ	195	261	GIII	116	пси	200	ASII	vai	DCI	шец	205	110	, 42	
E>	1756	C1 17	Tvc		Luc	Tlo	T.e.u	Δen		Lvs	Thr	Asp	Pro		Leu	Pro	Lvs
ъ 🔪	1757	СТУ	210	FIIC	цуз	110	шси	215	11011	1 10	****	p	220	501			-1-
E/	1760	Ser		Δan	Tle	Lvs	Len		Phe	Asp	Gln	Asn		Val	Leu	Leu	Glu
F>	1761		1110	non	110	1,5	230	Doa		F		235	1				240
P>	1764	Asn	Ser	Asn	Tle	Glu		Gln	Tvr	Leu	Asn		Arq	Ser	Gly	Asp	Ser
E>	1765		001			245	-1-		-1-		250		_		-	255	
.	1768	Ile	Leu	Pro	Glu		Tyr	Lys	Asn	Ala	Ile	Gly	Phe	Met	Pro	Asn	Leu
E>					260		-	-		265					270		
	1772	Leu	Ala	Tyr	Ala	Lys	Ala	Thr	Thr	Asp	Gln	Ser	Lys	Ile	Tyr	Ala	Arg
E>	1773			275					280					285			
	1776	Asn	Thr	Ile	Tyr	Gly	Asn	Ile	Tyr	Leu	Asp	Asn	Gln	Pro	Tyr	Asn	Pro
E>	1777		290					295					300				
	1780	Val	Val	Ile	Lys	Ile	Thr	Phe	Asn	Asn	Glu	Ala	Asp	Ser	Ala	Tyr	
E>	1781						310					315			_		320
	1784	Ile	Thr	Phe	Asn	Tyr	Ser	Trp	Thr	Lys		Tyr	Asp	Asn	Ile		Phe
E>	1785					325					330					335	
	1788	Asp	Ser	Thr		Phe	Thr	Ser									
E>	1789				340												
			<210> SEQ ID NO: 41														
			<211> LENGTH: 386														
			<212> TYPE: PRT														
			<pre><213> ORGANISM: adenoviridae <220> FEATURE:</pre>														
			<221> NAME/KEY: VARIANT														
		<222> LOCATION: (1)(386)															
	1/20	0 \222/ DOCATION: (1)(300)															

```
1799 <223> OTHER INFORMATION: Serotype 30 fiber protein
     1801 <220> FEATURE:
     1802 <221> NAME/KEY: MISC_FEATURE
     1803 <222> LOCATION: (23)
     1804 <223> OTHER INFORMATION: 'Xaa' at position 23 indicates unidentified amino acid due
                to unidentified nucleotide(s)
     1805
     1807 <220> FEATURE:
     1808 <221> NAME/KEY: MISC_FEATURE
     1809 <222> LOCATION: (43)
     1810 <223> OTHER INFORMATION: 'Xaa' at position 43 indicates unidentified amino acid due
                to Unidentified nucleotide(s)
     1813 <220> FEATURE:
     1814 <221> NAME/KEY: MISC_FEATURE
     1816 <222> LOCATION: (49)
     1817 <223> OTHER INFORMATION: 'Xaa' at position 49 indicates unidentified amino acid due
                to unidentified nucleotide(s)
     1818
     1820 <220> FEATURE:
     1821 <221> NAME/KEY: MISC_FEATURE
     1822 <222> LOCATION: (97)
     1823 <223> OTHER INFORMATION: 'Xaa' at position 97 indicates unidentified amino acid due
                to unidentified nucleotide(s)
     1824
     1826 <220> FEATURE:
     1827 <221> NAME/KEY: MISC_FEATURE
     1828 <222> LOCATION: (152)
     1829 <223> OTHER INFORMATION: 'Xaa' at position 152 indicates unidentified amino acid
                due to unidentified nucleotide(s)
     1832 <220> FEATURE:
     1833 <221> NAME/KEY: MISC_FEATURE ? only 186 amind acids in the sequence 1834 <222> LOCATION: (186). (786) ? only 186 amind acids in the sequence
     1835 <223> OTHER INFORMATION: 'Xaa' at position 186 indicates unidentified amino acid
                due to unidentified nucleotide(s)
     1836
     1838 <400> SEQUENCE: 41
     1840 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
E--> 1841
                                                                                               15
                                                                          10
W--> 1844 Lys Arg Ala Arg Pro Ser Xaa Asp Thr Phe Asn Pro Val Tyr Pro Tyr
                      20
                                           25
E--> 1845
W--> 1848 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Xaa Thr Pro Pro Phe Val
                                       40
E--> 1849
                  35
W--> 1852 Xaa Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
                                                        60
                                   55
     1856 Leu Ala Asp Pro Ile Ala Ile Thr Asn Gly Asp Val Ser Leu Lys Val
                                                    75
                               70
E--> 1857 65
     1860 Gly Gly Gly Leu Thr Val Glu Gln Asp Ser Gly Asn Leu Ser Val Asn
E--> 1861
W--> 1864 Xaa Lys Ala Pro Leu Gln Val Gly Thr Asp Lys Lys Leu Glu Leu Ala
                                           105
E--> 1865 .
                      100
     1868 Leu Ala Pro Pro Phe Asp Val Arg Asp Asn Lys Leu Ala Ile Leu Val
                                       120
     1872 Gly Asp Gly Leu Lys Val Ile Asp Arg Ser Ile Ser Asp Leu Pro Gly
```

```
E--> 1873
             130
                                 135
                                                     140
W--> 1876 Leu Leu Asn Tyr Leu Val Val Xaa Thr Gly Lys Gly Ile Gly Asn Glu
E--> 1877 145
                             150
                                                155
    1880 Glu Leu Lys Asn Asp Asp Gly Ser Asn Lys Gly Val Gly Leu Cys Val
E--> 1881
                     165
                                            170/
W--> 1884 Arg Ile Gly Glu Gly Gly Leu Thr Xaá Asp Asp Lys Gly Tyr Leu
                    180
                                        185
                                                             190
E--> 1885
    1888 Val Ala Trp Asn Asn Lys His Asp Ile Arg Thr Leu Trp Thr Thr Leu
E--> 1889
                 195
                                     200
    1892 Asp Pro Ser Pro Asn Cys Lys Ile Asp Ile Glu Lys Asp Ser Lys Leu
                                                     220
E--> 1893
             210
                                 215
    1896 Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser
                                                 235
E--> 1897 225
                             230
    1900 Leu Ile Ile Val Asn Gly Lys Phe Lys Ile Leu Asn Asn Lys Thr Asp
                         245
                                             250
E--> 1901
    1904 Pro Ser Leu Pro Lys Ser Phe Asn Ile Lys Leu Leu Phe Asp Gln Asn
E--> 1905
                                         265
                     260
    1908 Gly Val Leu Leu Glu Asn Ser Asn Ile Glu Lys Gln Tyr Leu Asn Phe
E--> 1909
                                     280
                 275
                                                         285
    1912 Arg Ser Gly Asp Ser Ile Leu Pro Glu Pro Tyr Lys Asn Ala Ile Gly
E--> 1913
             290
                                 295
                                                     300
    1916 Phe Met Pro Asn Leu Leu Ala Tyr Ala Lys Ala Thr Thr Asp Gln Ser
E--> 1917 305
                             310
    1920 Lys Ile Tyr Ala Arg Asn Thr Ile Tyr Gly Asn Ile Tyr Leu Asp Asn
                                             330
E--> 1921
                         325
    1924 Gln Pro Tyr Asn Pro Val Val Ile Lys Ile Thr Phe Asn Asn Glu Ala
                     340
                                         345
                                                             350
E--> 1925
    1928 Asp Ser Ala Tyr Ser Ile Thr Phe Asn Tyr Ser Trp Thr Lys Asp Tyr
E--> 1929 355
                                     360
    1932 Asp Asn Ile Pro Phe Asp Ser Thr Ser Phe Thr Phe Ser Tyr Ile Ala
E--> 1933 370
                                 375
                                                     380
    1936 Gln Glu
E--> 1937 385
    1939 <210> SEQ ID NO: 42
    1940 <211> LENGTH: 391
    1941 <212> TYPE: PRT
    1942 <213> ORGANISM: adenoviridae
    1944 <220> FEATURE:
    1945 <221> NAME/KEY: VARIANT
    1946 <222> LOCATION: (1)..(391)
    1947 <223> OTHER INFORMATION: Serotype 32 fiber protein
    1949 <400> SEQUENCE: 42
   1951 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
E--> 1952
                                                                                          15
    1955 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Ash Pro Val Tyr Pro Tyr
E--> 1956
                     20
                                         25
    1959 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val
                                     40
    1963 Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
```

```
E--> 1964
              50
                                  55
    1967 Leu Ala Asp Pro Ile Thr Ile Ala Asn Gly Asn Val Ser Leu Lys Val
E--> 1968 65
                              70
     1971 Gly Gly Gly Leu Thr Leu Glu Gln Asp Ser Gly Lys Leu Ile Val Asn
E--> 1972
                          85
     1975 Pro Lys Ala Pro Leu Gln Val Ala Asn Asp Lys Leu Glu Leu Ser Tyr
E--> 1976
                                          105
     1979 Ala Asp Pro Phe Glu Thr Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
E--> 1980 115
                                      120
     1983 His Gly Leu Lys Val Leu Asp Glu Lys Asn Ala Gly Gly Leu Lys Asp
E--> 1984 130
                                 135
                                                     140
     1987 Leu Ile Gly Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Val Glu
E--> 1988 145
                             150
                                                 155
     1991 Glu Leu Lys Asn Ala Asp Asn Thr Asn Arg Gly Val Gly Ile Asn Val
                         165
                                             170
     1995 Arg Leu Gly Lys Asp Gly Gly Leu Ser Phe Asp Lys Lys Gly Asp Leu
                      180
                                         185
     1999 Val Ala Trp Asn Lys His Asp Asp Arg Arg Thr Leu Trp Thr Thr Pro
                 195
                                     200
     2003 Asp Pro Ser Pro Asn Cys Thr Ile Asp Glu Glu Arg Asp Ser Lys Leu
                                 215
                                                     220
     2007 Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser
E--> 2008 225
                             230
                                                 235
     2011 Leu Leu Val Val Lys Gly Lys Phe Ser Asn Ile Asn Asn Asn Thr Asn
E--> 2012
                         245
                                             250
     2015 Pro Thr Asp Lys Lys Ile Thr Val Lys Leu Leu Phe Asn Glu Lys Gly
E--> 2016
                     260
                                         265
     2019 Val Leu Met Asp Ser Ser Ser Leu Lys Lys Glu Tyr Trp Asn Tyr Arg
                 275
                                     280
     2023 Asn Asp Asn Ser Thr Val Ser Gln Ala Tyr Asp Asn Ala Val Pro Phe
             290
                                 295
                                                     300
     2027 Met Pro Asn Ile Lys Ala Tyr Pro Lys Pro Thr Thr Asp Thr Ser Ala
E--> 2028 305
                             310
     2031 Lys Pro Glu Asp Lys Lys Ser Ala Ala Lys Arg Tyr Ile Val Ser Asn
E--> 2032
                         325
                                             330
     2035 Val Tyr Ile Gly Gly Leu Pro Asp Lys Thr Val Val Ile Thr Ile Lys
E--> 2036
                     340
                                         345
    2039 Leu Asn Ala Glu Thr Glu Ser Ala Tyr Ser Met Thr Phe Glu Phe Thr
E--> 2040 355
                                     360
     2043 Trp Ala Lys Thr Phe Glu Asn Leu Gln Phe Asp Ser Ser Phe Thr
E--> 2044
            370
    2047 Phe Ser Tyr Ile Ala Gln Glu
E--> 2048 385
     2050 <210> SEQ ID NO: 43
     2051 <211> LENGTH: 391
     2052 <212> TYPE: PRT
     2053 <213> ORGANISM: adenoviridae
    2055 <220> FEATURE:
    2056 <221> NAME/KEY: VARIANT
```

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\09182002\J040949.raw

2057 <222> LOCATION: (1)..(391) 2058 <223> OTHER INFORMATION: Serotype 33 fiber protein 2060 <400> SEQUENCE: 43 2062 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met E--> 2063 2066 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr 25 2070 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val 35 40 2074 Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys 55 2078 Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys Val 70 2082 Gly Gly Gly Leu Thr Leu Gln Glu Gly Ser Leu Thr Val Asn Pro Lys 2086 Ala Pro Leu Gln Leu Ala Asn Asp Lys Lys Leu Glu Leu Val Tyr Asp 105 2090 Asp Pro Phe Glu Val Ser Thr Asn Lys Leu Ser Leu Lys Val Gly His 2091 115 120 2094 Gly Leu Lys Val Leu Asp Asp Lys Ser Ala Gly Gly Leu Gln Asp Leu 135 140 2098 Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Ile Glu Asn 2099 145 150 155 2102 Leu Gln Asn Asp Asp Gly Ser Ser Arg Gly Val Gly Ile Asn Val Arg 165 170 2106 Leu Gly Thr Asp Gly Gly Leu Ser Phe Asp Arg Lys Gly Glu Leu Val 180 185 2110 Ala Trp Asn Arg Lys Asp Asp Arg Thr Leu Trp Thr Thr Pro Asp 195 200 2114 Pro Ser Pro Asn Cys Lys Ala Glu Thr Glu Lys Asp Ser Lys Leu Thr 215 220 2118 Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Ile 2119 225 230 2122 Ile Val Leu Lys Gly Lys Tyr Glu Phe Val Lys Lys Glu Thr Glu Pro 245 250 2126 Lys Ser Phe Asp Val Lys Leu Leu Phe Asp Ser Lys Gly Val Leu Leu 2127 260 265 270 2130 Pro Thr Ser Asn Leu Ser Lys Glu Tyr Trp Asn Tyr Arg Ser Tyr Asp 2131 275 280 2134 Asn Asn Ile Gly Thr Pro Tyr Glu Asn Ala Val Pro Phe Met Pro Asn 295 2138 Leu Lys Ala Tyr Pro Lys Pro Thr Lys Thr Ala Ser Asp Lys Ala Glu 310 315 2142 Asn Lys Ile Ser Ser Ala Lys Asn Lys Ile Val Ser Asn Phe Tyr Phe 325 330 2146 Gly Gly Gln Ala Tyr Gln Pro Gly Thr Ile Ile Ile Lys Phe Asn Glu 340 345 2150 Glu Ile Asp Glu Thr Cys Ala Tyr Ser Ile Thr Phe Asn Phe Gly Trp

360

355

```
2154 Gly Lys Val Tyr Asp Asn Pro Phe Pro Phe Asp Thr Thr Ser Phe Thr
     2155
             370
     2158 Phe Ser Tyr Ile Ala Gln Glu
     2159 385
     2161 <210> SEQ ID NO: 44
     2162 <211> LENGTH: 338
     2163 <212> TYPE: PRT
     2164 <213> ORGANISM: adenoviridae
     2166 <220> FEATURE:
     2167 <221> NAME/KEY: VARIANT
     2168 <222> LOCATION: (1)..(338)
     2169 <223> OTHER INFORMATION: Serotype 34 fiber protein
     2171 <400> SEQUENCE: 44
     2173 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
E--> 2174
                                                                                10
     2177 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
     2181 Glu Asp Glu Ser Thr Ser Gln His Pro Phe Ile Asn Pro Gly Phe Ile
                 35
                                     40
     2185 Ser Pro Asn Gly Phe Thr Gln Ser Pro Asp Gly Val Leu Thr Leu Lys
             50
                                 55 .
    2189 Cys Leu Thr Pro Leu Thr Thr Thr Gly Gly Ser Leu Gln Leu Lys Val
    2190 65
                             70
                                                 75
    2193 Gly Gly Leu Thr Val Asp Asp Thr Asp Gly Thr Leu Gln Lys Asn
                         85
    2197 Ile Arg Ala Thr Thr Pro Ile Thr Lys Asn Asn His Ser Val Glu Leu
                     100
                                         105
     2201 Thr Ile Gly Asn Gly Leu Glu Thr Gln His Asn Lys Leu Cys Ala Lys
    2202 115 .
                                     120
    2205 Leu Gly Asn Gly Leu Lys Phe Asn Asn Gly Asp Ile Cys Ile Lys Asp
                                 135
    2209 Ser Ile Asn Thr Leu Trp Thr Gly Ile Asn Pro Pro Pro Asn Cys Gln
    2210 145
                             150
                                                 155
    2213 Ile Val Glu Asn Thr Asn Thr Asn Asp Gly Lys Leu Thr Leu Val Leu
                         165
                                             170
    2217 Val Lys Asn Gly Gly Leu Val Asn Gly Tyr Val Ser Leu Val Gly Val
                    180
                                         185
    2221 Ser Asp Thr Val Asn Gln Met Phe Thr Gln Lys Thr Ala Asn Ile Gln
    2222 195
                                     200
    2225 Leu Arg Leu Tyr Phe Asp Ser Ser Gly Asn Leu Leu Thr Asp Glu Ser
                                 215
    2229 Asp Leu Lys Ile Pro Leu Lys Asn Lys Ser Ser Thr Ala Thr Ser Glu
    2230 225
                             230
                                                 235
    2233 Thr Val Ala Ser Ser Lys Ala Phe Met Pro Ser Thr Thr Ala Tyr Pro
                                             250
                         245
    2237 Phe Asn Thr Thr Arg Asp Ser Glu Asn Tyr Ile His Gly Ile Cys
                     260
                                         265
    2241 Tyr Tyr Met Thr Ser Tyr Asp Arg Ser Leu Phe Pro Leu Asn Ile Ser
         - 275
                                     280
```

```
2245 Ile Met Leu Asn Ser Arg Met Ile Ser Ser Asn Val Ala Tyr Ala Ile
                                                      300
                                 295
     2249 Gln Phe Glu Trp Asn Leu Asn Ala Ser Glu Ser Pro Glu Lys Gln His
                                                 315
                         310
    2253 Met Thr Leu Thr Thr Ser Pro Phe Phe Phe Ser Tyr Ile Ile Glu Asp
                          325
                                              330
    2254
    2257 Asp Asn
     2259 <210> SEQ ID NO: 45
     2260 <211> LENGTH: 338
     2261 <212> TYPE: PRT
     2262 <213> ORGANISM: adenoviridae
     2264 <220> FEATURE:
     2265 <221> NAME/KEY: VARIANT
     2267 <222> LOCATION: (1)..(338)
     2268 <223> OTHER INFORMATION: Serotype 35 fiber protein
     2270 <400> SEQUENCE: 45
     2272 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
E--> 2273
                                                                                       10
                                                  1
     2276 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
                                                              30
                      20
                                          25
     2280 Glu Asp Glu Ser Thr Ser Gln His Pro Phe Ile Asn Pro Gly Phe Ile
                                      40
     2284 Ser Pro Asn Gly Phe Thr Gln Ser Pro Asp Gly Val Leu Thr Leu Lys
                                  55
     2288 Cys Leu Thr Pro Leu Thr Thr Thr Gly Gly Ser Leu Gln Leu Lys Val
                              70
     2292 Gly Gly Gly Leu Thr Val Asp Asp Thr Asp Gly Thr Leu Gln Glu Asn
     2296 Ile Arg Ala Thr Ala Pro Ile Thr Lys Asn Asn His Ser Val Glu Leu
                                          105
                      100
     2300 Ser Ile Gly Asn Gly Leu Glu Thr Gln Asn Asn Lys Leu Cys Ala Lys
                                      120
                 115
     2304 Leu Gly Asn Gly Leu Lys Phe Asn Asn Gly Asp Ile Cys Ile Lys Asp
                                  135
     2308 Ser Ile Asn Thr Leu Trp Thr Gly Ile Asn Pro Pro Pro Asn Cys Gln
                                                  155
     2309 145
                              150
     2312 Ile Val Glu Asn Thr Asn Thr Asn Asp Gly Lys Leu Thr Leu Val Leu
                                              170
                          165
     2316 Val Lys Asn Gly Gly Leu Val Asn Gly Tyr Val Ser Leu Val Gly Val
                                          185
                      180
     2320 Ser Asp Thr Val Asn Gln Met Phe Thr Gln Lys Thr Ala Asn Ile Gln
                                      200
                  195
     2324 Leu Arg Leu Tyr Phe Asp Ser Ser Gly Asn Leu Leu Thr Glu Glu Ser
     2325
              210
                                  215
     2328 Asp Leu Lys Ile Pro Leu Lys Asn Lys Ser Ser Thr Ala Thr Ser Glu
                                                   235
                              230
     2332 Thr Val Ala Ser Ser Lys Ala Phe Met Pro Ser Thr Thr Ala Tyr Pro
                                              250
                          245
     2336 Phe Asn Thr Thr Thr Arg Asp Ser Glu Asn Tyr Ile His Gly Ile Cys
```

```
265
    2337
                    260
    2340 Tyr Tyr Met Thr Ser Tyr Asp Arg Ser Leu Phe Pro Leu Asn Ile Ser
                                                       285
    2341 275 280
    2344 Ile Met Leu Asn Ser Arg Met Ile Ser Ser Asn Val Ala Tyr Ala Ile
    2345 290
                               295
    2348 Gln Phe Glu Trp Asn Leu Asn Ala Ser Glu Ser Pro Glu Ser Asn Ile
    2349 305 310
                                               315
    2352 Met Thr Leu Thr Thr Ser Pro Phe Phe Phe Ser Tyr Ile Thr Glu Asp
                                            330
                     325
    2356 Asp Asn
    2358 <210> SEQ ID NO: 46
    2359 <211> LENGTH: 392
    2360 <212> TYPE: PRT
    2361 <213> ORGANISM: adenoviridae
    2363 <220> FEATURE:
    2364 <221> NAME/KEY: VARIANT
    2365 <222> LOCATION: (1)..(392)
    2366 <223> OTHER INFORMATION: Serotype 36 fiber protein
    2368 <400> SEQUENCE: 46
    2370 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
E--> 2371
                                                                                        15
    2374 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro Tyr
                                        25
                     20
    2378 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val
                                                       45
E--> 2379
                 35
                                    40
    2382 Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
                                55
    2386 Leu Ala Asp Pro Ile Ala Ile Val Asn Gly Asp Val Ser Leu Lys Val
                                                75
E--> 2387 65
                            70
    2390 Gly Gly Leu Thr Val Glu Gln Asp Ser Gly Lys Leu Lys Val Asn
                                            90
                        85
    2394 Pro Lys Ile Pro Leu Gln Val Val Asn Asp Gln Leu Glu Leu Ala Thr
                                        105
E--> 2395
                     100
    2398 Asp Lys Pro Phe Lys Ile Glu Asn Asn Lys Leu Ala Leu Asp Val Gly
                                    120
E--> 2399 115
    2402 His Gly Leu Lys Val Ile Asp Lys Thr Ile Ser Asp Leu Gln Gly Leu
                                135
E--> 2403 130
    2406 Val Gly Lys Leu Val Val Leu Thr Gly Val Gly Ile Gly Thr Glu Thr
                                                155
                            150
    2410 Leu Lys Asp Lys Asn Asp Lys Val Ile Gly Ser Ala Val Asn Val Arg
                                            170
E--> 2411
    2414 Leu Gly Lys Asp Gly Gly Leu Asp Phe Asn Lys Lys Gly Asp Leu Val
                                        185
                     180
    2418 Ala Trp Asn Arg Tyr Asp Asp Arg Arg Thr Leu Trp Thr Thr Pro Asp
                                    200
E--> 2419
                 195
    2422 Pro Ser Pro Asn Cys Lys Val Ser Glu Ala Lys Asp Ser Lys Leu Thr
                                                    220
                                215
    2426 Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Ser Val Ala Leu
                                                235
                             230
E--> 2427 225
```

```
2430 Leu Ile Val Lys Gly Lys Tyr Gln Thr Ile Ser Glu Ser Thr Ile Pro
                                             250
E--> 2431
                         245
    2434 Lys Asp Gln Arg Asn Phe Ser Val Lys Leu Met Phe Asp Glu Lys Gly
                                        265
E--> 2435 260
    2438 Lys Leu Leu Asp Lys Ser Ser Leu Asp Lys Glu Tyr Trp Asn Phe Arg
                                                         285
E--> 2439 275
                                     280
    2442 Ser Asn Asp Ser Val Val Gly Thr Ala Tyr Asp Asn Ala Val Pro Phe
                                                     300
             290
                               295
    2446 Met Pro Asn Leu Lys Ala Tyr Pro Lys Asn Thr Thr Thr Ser Ser Thr
E--> 2447 305
                             310
                                                 315
    2450 Asn Pro Asp Asp Lys Ile Ser Ala Gly Lys Lys Asn Ile Val Ser Asn
                                             330
                          325
E--> 2451
    2454 Val Tyr Leu Glu Gly Arg Val Tyr Gln Pro Val Ala Leu Thr Val Lys
                     340
                                          345
E--> 2455
     2458 Phe Asn Ser Glu Asn Asp Cys Ala Tyr Ser Ile Thr Phe Asp Phe Val
                                     360
          355
    2462 Trp Ser Lys Thr Tyr Glu Ser Pro Val Ala Phe Asp Ser Ser Ser Phe
                                                      380
E--> 2463 370
                                 375
     2466 Thr Phe Ser Tyr Ile Ala Gln Glu
E--> 2467 385
                              390
     2469 <210> SEQ ID NO: 47
     2470 <211> LENGTH: 380
     2471 <212> TYPE: PRT
     2472 <213> ORGANISM: adenoviridae
     2474 <220> FEATURE:
     2475 <221> NAME/KEY: VARIANT
     2476 <222> LOCATION: (1)..(380)
     2477 <223> OTHER INFORMATION: Serotype 37 fiber protein
     2479 <400> SEQUENCE: 47
     2481 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
E--> 2482
                                           1
                                                                                 10
     2485 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Ash Pro Val Tyr Pro Tyr
                                                              30
                     20
                                         25
     2489 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val
                                      40
     2493 Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
                                                      60
                                  55
     2497 Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys Val
                                                  75
                              70
     2501 Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro Lys
                                              90
     2505 Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr Asp
                                          105
     2506
                      100
     2509 Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly His
                115
                                      120
     2513 Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp Leu
                                                      140
                                  135
     2517 Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Asn
                                                  155
                              150
     2518 145
```

```
2521 Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val Arg
                     165
                                         170
2525 Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala Trp
2526
                 180
                                     185
2529 Asn Pro Lys Tyr Asp Leu Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser
                                 200
2533 Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu Val
                             215
                                                 220
2537 Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val
2538 225
                         230
                                             235
2541 Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys Ile
                     245
                                         250
2545 Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu Leu
                                     265
2549 Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly Asn
2550
             275
                                 280
2553 Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn
                             295
2557 Leu Val Ala Val Ser Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg Asp
                         310
2561 Ile Val Tyr Gly Asn Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Gly
                     325
                                         330
2565 Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile
                 340
                                     345
2569 Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe Glu
2570 355
                                 360
2573 Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
         370
                             375
2576 <210> SEQ ID NO: 48
2577 <211> LENGTH: 391
2578 <212> TYPE: PRT
2579 <213> ORGANISM: adenoviridae
2581 <220> FEATURE:
2582 <221> NAME/KEY: VARIANT
2583 <222> LOCATION: (1)..(391)
2584 <223> OTHER INFORMATION: Serotype 39 fiber protein
2586 <220> FEATURE:
2587 <221> NAME/KEY: MISC_FEATURE
2588 <222> LOCATION: (43)
2589 <223> OTHER INFORMATION: 'Xaa' at position 43 indicates an unidentified amino acid
          due to unidentified nucleotide(s)
2592 <220> FEATURE:
2593 <221> NAME/KEY: MISC_FEATURE
2594 <222> LOCATION: (49)
2595 <223> OTHER INFORMATION: 'Xaa' at position 49 indicates an unidentified amino acid
2596
          due to unidentified nucleotide(s)
2598 <220> FEATURE:
2599 <221> NAME/KEY: MISC_FEATURE
2600 <222> LOCATION: (97)
```

```
2601 <223> OTHER INFORMATION: 'Xaa' at position 97 indicates an unidentified amino acid
                due to unidentified nucleotide(s)
     2602
     2604 <220> FEATURE:
     2605 <221> NAME/KEY: MISC_FEATURE
     2606 <222> LOCATION: (192)
     2607 <223> OTHER INFORMATION: 'Xaa' at position 192 indicates an unidentified amino acid
                due to unidentified nucleotide(s)
     2610 <400> SEQUENCE: 48
     2612 Ser Cys Ser Cys Pro Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
E--> 2613
                                                                                      10
     2616 Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Ash Pro Val Tyr Pro Tyr
     2617
                                                                 30
  ^{\prime} > ^{\prime} > ^{\prime} 2620 Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Xaa Thr Pro Pro Phe Val
     2621
                                        40
                                                     ė
	ilde{\mathsf{V}}^{	extsf{-}}\mathsf{-}\mathsf{>} 2624 Xaa Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
                                    55
                                                         60
     2628 Leu Ala Asp Pro Ile Thr Ile Ala Asn Gly Asn Val Ser Leu Lys Val
     2629 65
                               70
                                                    75
     2632 Gly Gly Gly Leu Thr Leu Glu Gln Asp Ser Gly Lys Leu Ile Val Asn
                           85
     2636 Xaa Lys Ala Pro Leu Gln Val Ala Asn Asp Lys Leu Glu Leu Ser Tyr
                      100
                                            105
     2640 Ala Asp Pro Phe Glu Thr Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
                  115
                                        120
     2644 His Gly Leu Lys Val Leu Asp Glu Lys Asn Ala Gly Gly Leu Lys Asp
                                    135
     2648 Leu Ile Gly Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Val Glu
                               150
     2649 145
                                                    155
     2652 Glu Leu Lys Asn Ala Asp Asn Thr Asn Arg Gly Val Gly Ile Asn Val
     2653
                           165
                                                170
     2656 Arg Leu Gly Lys Asp Gly Gly Leu Ser Phe Asp Lys Lys Gly Asp Xaa
     2657
                       180
                                            185
     2660 Val Ala Trp Asn Lys His Asp Asp Arg Arg Thr Leu Trp Thr Thr Pro
                  195
                                        200
                                                             205
     2664 Asp Pro Ser Pro Asn Cys Thr Ile Asp Glu Glu Arg Asp Ser Lys Leu
                                    215
                                                         220
     2668 Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser
                               230
                                                     235
     2672 Leu Leu Val Val Lys Gly Lys Phe Ser Asn Ile Asn Asn Asn Thr Asn
                                                250
     2676 Pro Thr Asp Lys Lys Ile Thr Val Lys Leu Leu Phe Asn Glu Lys Gly
     2677
                       260
                                            265
     2680 Val Leu Met Asp Ser Ser Ser Leu Lys Lys Glu Tyr Trp Asn Tyr Arg
                                        280
     2684 Asn Asp Asn Ser Thr Val Ser Gln Ala Tyr Asp Asn Ala Val Pro Phe
     2685
                                    295
     2688 Met Pro Asn Ile Lys Ala Tyr Pro Lys Pro Thr Thr Asp Thr Ser Ala
     2689 305
                                                    315
                               310
     2692 Lys Pro Glu Asp Lys Lys Ser Ala Ala Lys Arg Tyr Ile Val Ser Asn
```

DATE: 09/18/2002

TIME: 14:46:57

Input Set : A:\Sequence Listing.txt Output Set: N:\CRF4\09182002\J040949.raw 335 2693 325 330 2696 Val Tyr Ile Gly Gly Leu Pro Asp Lys Thr Val Val Ile Thr Ile Lys 340 345 2700 Leu Asn Ala Glu Thr Glu Ser Ala Tyr Ser Met Thr Phe Glu Phe Thr 355 360 365 2701 2704 Trp Ala Lys Thr Phe Glu Asn Leu Gln Phe Asp Ser Ser Ser Phe Thr 375 380 370 2708 Phe Ser Tyr Ile Ala Gln Glu 2709 385 2711 <210> SEQ ID NO: 49 2712 <211> LENGTH: 339 2713 <212> TYPE: PRT 2714 <213> ORGANISM: adenoviridae 2716 <220> FEATURE: 2717 <221> NAME/KEY: VARIANT 2718 <222> LOCATION: (1)..(339) 2719 <223> OTHER INFORMATION: Serotype 39 fiber protein 2721 <400> SEQUENCE: 49 2723 Ile Arg Ile Ser Pro Ser Ser Leu Pro Pro Leu Ser Pro Pro Met Asp E--> 2724 10 2727 Ser Lys Thr Ser Pro Leu Gly Cys Tyr His Ser Asn Trp Leu Thr Gln 20 2728 2731 Ser Pro Ser Pro Met Gly Met Ser His Ser Arg Trp Glu Gly Gly Ser 2732 2735 Pro Trp Gln Glu Gly Thr Gly Asp Leu Lys Val Asn Ala Lys Ser Pro 55 2739 Leu Gln Val Ala Thr Asn Lys Gln Leu Glu Ile Ala Leu Ala Lys Pro 2740 65 2743 Phe Glu Glu Lys Asp Gly Lys Leu Ala Leu Lys Ile Gly His Gly Leu 90 2747 Ala Val Val Asp Glu Asn His Thr His Leu Gln Ser Leu Ile Gly Thr 105 2748 100 2751 Leu Val Ile Leu Thr Gly Lys Gly Ile Gly Thr Gly Arg Ala Glu Ser 120 2755 Gly Gly Thr Ile Asp Val Arg Leu Gly Ser Gly Gly Leu Ser Phe 130 135 2759 Asp Lys Asp Gly Asn Leu Val Ala Trp Asn Lys Asp Asp Asp Arg Arg 2760 145 150 155 2763 Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Lys Ile Asp Gln 175 165 170 2767 Asp Lys Asp Ser Lys Leu Thr Phe Val Leu Thr Lys Cys Gly Ser Gln 2768 180 185 2771 Ile Leu Ala Asn Met Ser Leu Leu Val Val Lys Gly Lys Phe Ser Met 200 205 195 2775 Ile Asn Asn Lys Val Asn Gly Thr Asp Asp Tyr Lys Lys Phe Thr Ile 215 220 2776 210 2779 Lys Leu Leu Phe Asp Glu Lys Gly Val Leu Leu Lys Asp Ser Ser Leu 235 2783 Asp Lys Glu Tyr Trp Asn Tyr Arg Ser Asn Asn Asn Asn Val Gly Ser Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/040,949

explanation is presented in the <220> to <223> fields of

2784					245					250					255	
2787	Ala	Tyr	Glu	Glu	Ala	Val	Gly	Phe	Met	Pro	Ser	Thr	Thr	Ala	Tyr	Pro
2788		-		260					265					270		
2791	Lys	Pro	Pro	Thr	Pro	Pro	Thr	Asn	Pro	Thr	Thr	Pro	Leu	Glu	Lys	Ser
2792			275					280					285			
2795	Gln	Ala	Lys	Asn	Lys	Tyr	Val	Ser	Asn	Val	Tyr	Leu	Gly	Gly	Gln	Ala
2796		290					295					300				
2799	Gly	Asn	Pro	Val	Ala	Thr	Thr	Val	Ser	Phe	Asn	Lys	Glu	Thr	Gly	Cys
2800						310					315					320
2803	Thr	Tyr	Ser	Ile	Thr	Phe	Asp	Phe	Ala	Trp	Asn	Lys	Thr	Tyr		Asn
2804					325					330					335	
2807	Val	Gln	Cys													

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\09182002\J040949.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

```
Seq#:30; Line(s) 627,663
Seq#:31; Line(s) 735
Seq#:32; Line(s) 878
Seq#:33; Line(s) 989
Seq#:34; Line(s) 1077
Seq#:35; Line(s) 1176
Seq#:36; Line(s) 1276
Seq#:37; Line(s) 1393
Seq#:38; Line(s) 1500
Seq#:39; Line(s) 1597
Seq#:40; Line(s) 1705
Seq#:41; Line(s) 1841
Seq#:42; Line(s) 1952
Seq#:43; Line(s) 2063
Seq#:44; Line(s) 2174
Seq#:45; Line(s) 2273
Seq#:46; Line(s) 2371
Seq#:47; Line(s) 2482
Seq#:48; Line(s) 2613
Seq#:49; Line(s) 2724
Seq#:50; Line(s) 2828
Seq#:51; Line(s) 2947
Seq#:52; Line(s) 3042
Seq#:53; Line(s) 3141
Seq#:54; Line(s) 3240
Seq#:55; Line(s) 3339
Seq#:56; Line(s) 3450
Seg#:57; Line(s) 3555
Seq#:58; Line(s) 3666
```

VERIFICATION SUMMARY PATENT APPLICATION: US/10/040,949 DATE: 09/18/2002 TIME: 14:46:58

```
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:69 M:283 W: Missing Blank Line separator, <220> field identifier
L:108 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:5
L:627 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:30
M:332 Repeated in SeqNo=30
L:735 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
L:877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:878 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:16
L:885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:32
L:889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:48
L:973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:384
L:989 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:33
L:1077 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:34
L:1176 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:1276 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:1393 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37
L:1424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:128
L:1500 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
L:1597 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
L:1705 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
M:332 Repeated in SeqNo=40
L:1841 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
L:1844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:16
M:332 Repeated in SeqNo=41
L:1848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:32
L:1852 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:48
L:1864 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:96
L:1876 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:144
L:1884 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:176
L:1952 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
M:332 Repeated in SeqNo=42
L:2063 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
L:2174 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
L:2273 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
L:2371 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
M:332 Repeated in SeqNo=46
L:2482 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:47
L:2613 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:48
L:2620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:32
L:2624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:48
L:2636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:96
L:2656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:176
L:2724 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:49
L:2828 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:50
M:332 Repeated in SegNo=50
L:2883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:224
L:2946 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/040,949
DATE: 09/18/2002
TIME: 14:46:58

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\09182002\J040949.raw

L:2947 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:51 M:332 Repeated in SeqNo=51 L:3002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:224 L:3042 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:52 M:332 Repeated in SeqNo=52 L:3141 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:53 M:332 Repeated in SeqNo=53 L:3240 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:54 M:332 Repeated in SeqNo=54 L:3339 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:55 M:332 Repeated in SeqNo=55 L:3450 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:56 L:3555 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:57 M:332 Repeated in SeqNo=57 L:3618 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:256 L:3666 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:58 M:332 Repeated in SeqNo=58

Raw Sequence Listing Error Summary

ERROR DETECTED	suggested correction serial number: 10/040, 949
attn: new rules case	s: please disregard english "alpha" headers, which were inserted by Pto Software
Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
0Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
1Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See. 1.823 of Sequence Rules)
2PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
3Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

. . .